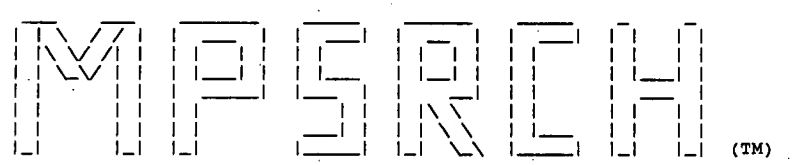
****



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Dec 31 06:54:38 1998; MasPar time 1797.76 Seconds
1522.512 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-16
Description: (1-1242) from US08765588.seq
Perfect Score: 1242
N.A. Sequence: 1 gcacgagctcaggccgtcgc.....aaaaaaaaaaaaaaaaaaaa 1242
Comp: cgtgctcgagtccggcagcg.....tttttttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl55
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
Database: genbank107
15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
32:gb_un 33:gb_vi

Statistics: Mean 11.947; Variance 15.062; scale 0.793

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1015	81.7	1236	28	MMU43836	Mus musculus VEGF-rela	0.00e+00
2	772	62.2	896	28	MMU52820	Mus musculus vascular	4.97e-242
3	537	43.2	1079	25	HSU43368	Human VEGF related fac	2.06e-162
4	535	43.1	755	27	HSU52819	Human vascular endothe	9.76e-162
5	509	41.0	886	21	I36625	Sequence 1 from patent	5.79e-153
6	403	32.4	795	28	MMU48800	Mus musculus vascular	2.63e-117
7	400	32.2	567	28	MMU43837	Mus musculus VEGF-rela	2.66e-116
8	398	32.0	565	21	I36626	Sequence 4 from patent	1.25e-115
9	380	30.6	405	21	I36628	Sequence 8 from patent	1.34e-109
10	319	25.7	349	28	AF032925	Rattus norvegicus vasc	3.15e-89
11	316	25.4	567	25	HSU43369	Human VEGF related fac	3.14e-88
12	316	25.4	570	21	I36629	Sequence 10 from paten	3.14e-88
13	316	25.4	570	25	HSU48801	Human vascular endothe	3.14e-88
14	296	23.8	591	21	I36627	Sequence 6 from patent	1.40e-81
15	282	22.7	453	28	AF022952	Rattus norvegicus vasc	6.19e-77
16	127	10.2	580	28	MMU80602	Mus musculus novel unk	1.86e-26
17	77	6.2	632	27	HSU80601	Human novel unknown ge	4.76e-11
18	65	5.2	7218	21	I66494	Sequence 14 from paten	1.58e-07
19	54	4.3	226	19	AF022179	Oryctolagus cuniculus	2.10e-04
20	52	4.2	576	25	S82167	simVEGF165-vascular en	7.54e-04
c 21	52	4.2	7218	21	I66494	Sequence 14 from paten	7.54e-04
22	50	4.0	576	21	A64392	Sequence 5 from Patent	2.67e-03
23	50	4.0	630	27	HSA010438	Homo sapiens mRNA for	2.67e-03
24	50	4.0	649	25	HSVEGF	H.sapiens vegf gene fo	2.67e-03
25	50	4.0	774	10	E11017	A part of pSU 2 includ	2.67e-03
26	50	4.0	774	21	E13332	cDNA encoding vascular	2.67e-03
27	50	4.0	774	21	E13215	Human mRNA for vascula	2.67e-03
28	50	4.0	815	27	S85192	Homo sapiens vascular	2.67e-03
29	50	4.0	990	25	HUMEGFAA	Human heparin-binding	2.67e-03
30	50	4.0	1195	25	HUMVPF	Human vascular permeab	2.67e-03
31	50	4.0	1649	21	A64396	Sequence 9 from Patent	2.67e-03
32	50	4.0	1664	21	A64404	Sequence 17 from Paten	2.67e-03
33	50	4.0	1787	21	A64394	Sequence 7 from Patent	2.67e-03
34	50	4.0	1790	21	A64398	Sequence 11 from Paten	2.67e-03
35	50	4.0	1790	21	A64400	Sequence 13 from Paten	2.67e-03
36	50	4.0	1832	21	A64402	Sequence 15 from Paten	2.67e-03
37	48	3.9	3166	27	AF022375	Homo sapiens vascular	9.31e-03
38	46	3.7	573	19	SSVEGF	S.scrofa mRNA for vasc	3.21e-02
39	45	3.6	1325	25	HUMCYCD1	Human cyclin D (cyclin	5.92e-02
c 40	44	3.5	307	30	G37984	c3m58 Plasmodium falci	1.09e-01
41	44	3.5	495	28	GPIVEGFA	Guinea pig vascular en	1.09e-01
42	44	3.5	802	19	BOVVEGFB	Bovine vascular endoth	1.09e-01
43	44	3.5	934	19	BOVVEGFA	Bovine vascular endoth	1.09e-01
44	44	3.5	1536	19	BOVEGFA	Bovine heparin-binding	1.09e-01
45	44	3.5	74371	26	AC005369	Homo sapiens chromosom	1.09e-01

ALIGNMENTS

RESULT 1
LOCUS MMU43836 1236 bp mRNA ROD 04-DEC-1996
DEFINITION Mus musculus VEGF-related factor mvrf186 precursor mRNA, complete cds.
ACCESSION U43836
NID g1703480
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1236)
AUTHORS Townson,S., Lagercrantz,J., Grimmond,S., Silins,G., Nordenskjold,M., Weber,G. and Hayward,N.
TITLE Characterization of the murine VEGF-related factor gene
JOURNAL Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
MEDLINE 96183052
REFERENCE 2 (bases 1 to 1236)
AUTHORS Hayward,N.K.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental Oncology Unit, Queensland Institute of Medical Research, Bancroft Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029, Australia
COMMENT On Dec 4, 1996 this sequence version replaced gi:1314333.
FEATURES Location/Qualifiers
source 1. .1236
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="m175-m1"
/clone_lib="Stratagene unizap neonatal whole brain cDNA library"
/tissue_type="whole brain"
/dev_stage="neonatal"
CDS 193. .816
/note="VEGF-related factor"

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MPSRCH (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Dec 31 07:25:10 1998; MasPar time 1622.48 Seconds
1370.828 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-16
Description: (1-1242) from US08765588.seq
Perfect Score: 1242
N.A. Sequence: 1 gcacgagctcaggccgtcgc.....aaaaaaaaaaaaaaaaaaaa 1242
Comp: cgtgctcgagtccggcagcg.....ttttttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est55
1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
Database: genbank-est107
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.844; Variance 6.260; scale 1.892

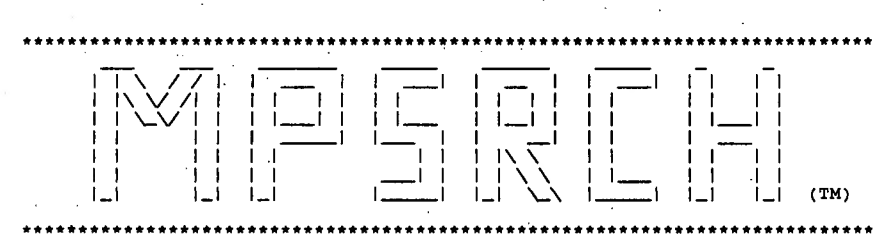
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	464	37.4	491	18	AI155033	ud78b11.r1 Soares mous	0.00e+00
2	402	32.4	412	20	W50682	md04b05.r1 Soares mous	6.14e-283
3	402	32.4	415	20	W71063	me31e02.r1 Soares mous	6.14e-283
4	380	30.6	410	17	AI117413	ub78g01.r1 Soares mous	2.20e-265
5	375	30.2	381	23	AA073557	mm94h03.r1 Stratagene	2.13e-261
6	362	29.1	389	18	AI174183	uc07b07.r1 Soares mous	4.81e-251
7	351	28.3	445	8	AA292448	zt29f01.r1 Soares ovar	2.71e-242
8	337	27.1	450	29	AF046494	Mus musculus clone OST	3.62e-231
9	331	26.7	415	24	AA310070	EST180930 Jurkat T-cel	2.10e-226
10	287	23.1	298	6	AA433107	vd94f08.r1 Soares mous	1.42e-191
11	234	18.8	531	6	AA434485	zw31a04.r1 Soares ovar	6.39e-150
12	229	18.4	423	23	AA073660	mm94g06.r1 Stratagene	5.17e-146
13	213	17.1	232	10	AA416146	vf36e10.r1 Soares mous	1.54e-133
14	203	16.3	341	16	H39505	yo54a11.r1 Homo sapien	9.10e-126
15	198	15.9	231	23	AA117672	mo61a06.r1 Stratagene	6.85e-122
16	197	15.9	312	16	R90829	yn02g09.r1 Homo sapien	4.08e-121
17	138	11.1	553	11	AA082818	zn25d01.r1 Stratagene	6.17e-76
18	119	9.6	523	21	AA040843	zk47h01.r1 Soares preg	1.07e-61
19	108	8.7	374	22	AA182397	zp36a04.r1 Stratagene	1.49e-53
c 20	104	8.4	565	10	AA633535	np66d06.s1 NCI_CGAP_Br	1.29e-50
21	100	8.1	118	10	AA419103	zv34a01.r1 Soares ovar	1.08e-47
22	98	7.9	225	5	T08411	EST06302 Homo sapiens	3.09e-46
c 23	98	7.9	566	18	AI141331	oy51f06.s1 NCI_CGAP_Br	3.09e-46
c 24	82	6.6	502	13	AA843665	ak08g12.s1 Soares para	9.80e-35
c 25	75	6.0	493	6	AA434389	zw31a04.s1 Soares ovar	8.31e-30
c 26	69	5.6	148	22	AA172960	ms58b01.r1 Life Tech m	1.20e-25
c 27	68	5.5	88	15	AA917955	ol68h05.s1 NCI_CGAP_Ki	5.86e-25
28	67	5.4	297	16	R88630	ym95c03.r1 Homo sapien	2.84e-24
29	65	5.2	148	22	AA172960	ms58b01.r1 Life Tech m	6.57e-23
c 30	61	4.9	252	12	AA754459	97SN1787 Rice Immature	3.31e-20
c 31	59	4.8	490	12	AA741539	ob29c01.s1 NCI_CGAP_Ki	7.18e-19
32	57	4.6	252	12	AA754459	97SN1787 Rice Immature	1.52e-17
c 33	56	4.5	247	12	AA754458	97SN1784 Rice Immature	6.94e-17
c 34	56	4.5	469	13	AA843530	ak08b11.s1 Soares para	6.94e-17
c 35	54	4.3	395	12	AA742966	ny15d03.s1 NCI_CGAP_GC	1.41e-15
36	50	4.0	211	9	AA592343	vo27a01.r1 Barstead mo	5.38e-13
37	50	4.0	247	12	AA754458	97SN1784 Rice Immature	5.38e-13
38	50	4.0	289	20	N87395	L3771F Fetal heart, La	5.38e-13
39	49	3.9	210	7	AA510867	vh55d06.r1 Soares mous	2.33e-12
40	48	3.9	269	24	AA266368	mz64g10.r1 Soares mous	9.99e-12
41	45	3.6	307	23	AA230517	mw06b08.r1 Soares mous	7.47e-10
42	45	3.6	472	26	B47188	HS-1068-B1-E11-MR.abi	7.47e-10
43	44	3.5	146	22	AA162025	mn41c01.r1 Beddington	3.08e-09
44	44	3.5	280	19	OSU37971	Oryza sativa clone pFD	3.08e-09
c 45	44	3.5	316	12	AA761367	nz24h01.s1 NCI_CGAP_GC	3.08e-09

ALIGNMENTS

RESULT 1
LOCUS AI155033 491 bp mRNA EST 30-SEP-1998
DEFINITION ud78b11.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone 1476957 5' similar to TR:Q64290 Q64290 VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN ;, mRNA sequence.
ACCESSION AI155033
NID g3683502
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 491)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:925313
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES Location/Qualifiers
source 1. .491
/organism="Mus musculus"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary



MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Dec 31 07:52:47 1998; MasPar time 190.02 Seconds
889.270 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-16
Description: (1-1242) from US08765588.seq
Perfect Score: 1242
N.A. Sequence: 1 gcacgagctcaggccgtcgc.....aaaaaaaaaaaaaaaaaaaa 1242
Comp: cgtgctcgagtccggcagcg.....tttttttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.362; Variance 8.021; scale 1.167

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1242	100.0	1242	23	T13809	Murine VRF186 cDNA.	0.00e+00
2	606	48.8	624	28	T37914	VEGF-B186 coding sequ	1.64e-280
3	575	46.3	1141	23	T13810	Murine VRF167 cDNA.	5.04e-265
4	537	43.2	1094	23	T33610	Vascular endothelial	4.67e-246
5	509	41.0	886	28	T37909	Partial VEGF-B coding	4.28e-232
6	488	39.3	624	28	T37915	VEGF-B186 coding sequ	1.24e-221
7	483	38.9	666	31	T44071	Human vascular endoth	3.85e-219
8	398	32.0	565	28	T37910	Adult heart VEGF-B167	6.87e-177
9	380	30.6	405	28	T37912	VEGF-B112 coding sequ	5.78e-168
10	316	25.4	570	28	T37913	Fibrosarcoma VEGF-B16	2.56e-136
11	315	25.4	858	23	T33612	Vascular endothelial	7.98e-136
12	314	25.3	993	23	T33611	Vascular endothelial	2.49e-135
13	296	23.8	591	28	T37911	Adult heart VEGF-B174	1.84e-126
14	259	20.9	910	23	T33613	Vascular endothelial	2.79e-108
15	62	5.0	1550	28	T37916	VEGF-B promoter fragm	1.54e-14
16	50	4.0	467	22	T17739	VEGF121 Cys+4 coding	2.28e-09
17	50	4.0	473	17	Q99080	cDNA encoding human v	2.28e-09
18	50	4.0	498	2	Q10797	Human vascular endoth	2.28e-09
19	50	4.0	576	37	T95839	DNA for vascular endo	2.28e-09
20	50	4.0	599	22	T17748	VEGF165 Cys+2 coding	2.28e-09
21	50	4.0	599	22	T17747	VEGF165 Cys+4 coding	2.28e-09
22	50	4.0	605	22	T17614	VEGF165 coding sequen	2.28e-09
23	50	4.0	605	17	Q99081	cDNA encoding human v	2.28e-09
24	50	4.0	649	23	T33609	Vascular endothelial	2.28e-09
25	50	4.0	774	32	T79139	Human vascular endoth	2.28e-09
26	50	4.0	774	33	T85644	Antisense inhibitory	2.28e-09
27	50	4.0	774	36	T95393	Human vascular endoth	2.28e-09
28	50	4.0	774	39	V15102	Human vascular endoth	2.28e-09
29	50	4.0	989	2	Q07006	Clone lambda.vegf.21	2.28e-09
30	50	4.0	1154	22	T35743	SAP-AlaMet-VEGF121 co	2.28e-09
31	50	4.0	1286	22	T35741	SAP-AlaMet-VEGF165 co	2.28e-09
32	50	4.0	1299	22	T17785	SAP(Gly4Ser)VEGF165 c	2.28e-09
33	50	4.0	1395	22	T35740	VEGF165-AlaMet-SAP co	2.28e-09
34	50	4.0	1538	22	T35745	SAP-AlaMet-VEGF121(Gl	2.28e-09
35	50	4.0	1557	22	T17789	SAP(Gly4Ser)VEGF121(G	2.28e-09
36	50	4.0	1595	22	T35751	SAP(Gly4Ser)2VEGF121(	2.28e-09
37	50	4.0	1649	37	T95831	DNA for VEGF/CPG2 fus	2.28e-09
38	50	4.0	1664	37	T95835	DNA for VEGF/CPG2 fus	2.28e-09
39	50	4.0	1787	37	T95830	DNA for VEGF/CPG2 fus	2.28e-09
40	50	4.0	1790	37	T95832	DNA for VEGF/CPG2 fus	2.28e-09
41	50	4.0	1802	22	T35748	SAP-AlaMet-VEGF165(Gl	2.28e-09
42	50	4.0	1808	22	T35752	SAP-GlySer-VEGF165(Gl	2.28e-09
43	50	4.0	1809	22	T17790	SAP(Gly4Ser)VEGF165(G	2.28e-09
44	50	4.0	1823	22	T35750	SAP-AlaMet-VEGF165(Gl	2.28e-09
45	50	4.0	1873	39	V15103	Human vascular endoth	2.28e-09

ALIGNMENTS

```
RESULT    1
ID   T13809 standard; cDNA; 1242 BP.
AC   T13809;
DT   30-NOV-1996  (first entry)
DE   Murine VRF186 cDNA.
KW   VRF; vascular endothelial growth factor; VEGF; SOM175; neuron;
KW   astroglial proliferation; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   cds             166..789
FT                   /*tag= a
FT   signal_peptide  166..228
FT                   /*tag= b
FT   mat_peptide     229..786
FT                   /*tag= c
FT   exon            576..676
FT                   /*tag= d
FT                   /note= "exon 6, deleted in VRF169"
FT   repeat_region   1163..1176
FT                   /*tag= e
FT                   /note= "polymorphic AC repeat region"
FT   polya_signal    1186..1191
FT                   /*tag= f
PN   WO9627007-A1.
PD   06-SEP-1996.
PF   22-FEB-1996; AU0094.
PR   02-MAR-1995; AU-001457.
PR   20-NOV-1995; AU-006647.
PR   22-DEC-1995; AU-007274.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Grimmond S,  Hayward NK,  Larsson C,  Nordenskjold M;
PI   Weber G;
DR   WPI; 96-412774/41.
DR   P-PSDB; W00863.
PT   New growth factor related to vascular endothelial growth factor -
PT   useful for inducing astroglial proliferation and promoting neuronal
PT   survival
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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Dec 31 10:31:17 1998; MasPar time 56.32 Seconds
1028.601 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-16
Description: (1-1242) from US08765588.seq
Perfect Score: 1242
N.A. Sequence: 1 gcacgagctcaggccgtcgc.....aaaaaaaaaaaaaaaaaaaa 1242
Comp: cgtgctcgagtccggcagcg.....ttttttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 8.877; Variance 6.415; scale 1.384

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	509	41.0	886	1	US-08-469-	Sequence 1, Applicatio	4.12e-277
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ALIGNMENTS

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CC   Sequence 1, Application US/08469427A
CC   Patent No. 5607918
CC    GENERAL INFORMATION:
CC      APPLICANT:  Eriksson, Ulf
CC      APPLICANT:  Olofsson, Birgitta
CC      APPLICANT:  Alitalo, Kari
CC      APPLICANT:  Pajusola, Katri
CC      TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC      TITLE OF INVENTION:  DNA CODING THEREFOR
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Evenson, McKeown, Edwards & Lenahan
CC        STREET:  1200 G Street, N.W., Suite 700
CC        CITY:  Washington
CC        STATE:  DC
CC        ZIP:  20005
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/469,427A
CC        FILING DATE:  06-JUN-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/397,651
CC        FILING DATE:  01-MAR-1995
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Evans, Joseph D
CC        REGISTRATION NUMBER:  26,269
CC        REFERENCE/DOCKET NUMBER:  41979cp2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (202) 628-8800
CC        TELEFAX:  (202) 628-8844
CC     INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  886 base pairs
CC        TYPE:  nucleic acid
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